

QY	206	CGCTCGGTTTCCACATTTCAACCAAACTCTGCTCGAAGAGCGAGATGATGATGAGCAAG	207
Db	1151	CCCTGGCCAGCACTTGACGACTCCATGCGCCAGACAGTACGGCAGGGGTCAATGGCCCGCG	1210
QY	266	AGGCATCGCTAAGACATGGCATGTGATTCCTCGAGCCGCACTATACACATCATCAACCTCC	325
Db	1211	ACGGACGGCGCCCTGGCCAGGACATGGTTCTTGAGCCCGATGATGAAACATACCGCGGTGC	1270
QY	326	CTCTCGGTGGACGTTGGCTTCGATCGATGTGTGTGAGATGATCCGTTCTGCGCGGCTTGGGAG	385
Db	1271	CACACGGCGGCGGAACTACGACGACTTTCAGCAGGAGACCCCTGTGGTCTCTTGCGCACCG	1330
QY	386	CTGCGGCTCTATCCGGGCAATTAGAGCACTGGAGTGGAGGTATGATCAAGCACTTTT	445
Db	1331	CGGTGCGCCAGTCAAGGGCATTCAGGGGTGCGGCTCTGATGACCAACGCGCAAGCACTTGG	1390
QY	446	TGTGCATATGATCAGAGGACAGGGCATGATGTGTGTCAGAGCATCTGCACGGAGCGGCTC	505
Db	1391	CGGCCAACACACGAGAGAACCAACGCTTCAGCTCAACGCGACAGTTCGACAGGACACGCG	1450
QY	506	TTCGGTAATCTAAGCACTCCGCTTCAGATGTGTGTGTCGAGATCTCCACGCGGGGTGCT	565
Db	1451	TTCGGAGATCACTGTTCCCGGCTTCAG---GGTCTCTGAAGGCGCGGCGGGCTCTCT	1507

QY	566	TCATGACGGCGATCAATGATGCATGTCGTGTCAGCGAAGACCTTAATATCTTG	625
Db	1508	TCATGTGTGCTATTAACGGCGATCAAGCGGACCGCTCTCGCGCACGACGACTCTCTA	1567
QY	626	ATGGGATGCTTGGAAAGAAATGGGGTTGGGATGGGCTTAATCATGAGCACTGGTACGGCA	685
Db	1568	ACAACTGCTGTGGCGACGGCAGTGGGGCTTCCAGGGCTGGGTGATGTCCGATGTGCTGCCA	1627
QY	686	CATACAGTACCAACAAGACCGTGTGGGAGGGCCGTGACGCTCGAGATGTCCCGACCTCCAC	745
Db	1628	C----CCGGGGCACGGACGCCATCAACAAAGGGCTCTGCACAGAGAT---GGGCTGCGAG	1687
QY	746	GCTTCGGAGGAAACACTCAAGTTCAACGCTTCCAAAGGAAAGCCCTTATTCACAGTCA	805
Db	1681	CTTCCCGGGGACATCCCGCCGGGAGAGCCCTCGCCCGCCCAAGTTCTTCGGTGCAGCG	1744
QY	806	TTGACCAAGGGGCTTGGGAAATCTTCTAGTTTCGTCAAGATGTGCTGCTCCGAGTGA	865
Db	1741	CTGA-----AGCAGGGCTGCTGAACGGCACGGTCCCGAAGGCGG	1780
QY	866	CGGAGACGGCCCCGAGACGACTGTCAACAACACCCCCGAAGCGGACGCTCTCTCCGA	925
Db	1781	CGGTGACGGGGTGGCGGAGGGATCTGTCAACAGATGAGCAAGTTCCGTTCTGCTCTG	1844
QY	926	AGTTGGCAGAGGGGCACTGCTGCTGTGAAGACGAAACAAGTTTGTCCCTTGAGCA	985
Db	1841	CGACTCTGGGCGCCCCCGCCAGCGGTGACAAAGGGGGGCCCCAGCGGTGTCGCCCAAG	1900
QY	986	AGAAAGAAAGACGCTGATTTGTGGCCCCCAAGCGGACGACATACACAGGGGAG	1045
Db	1901	TGCGCGGAAAGGGCGGGTGTCTCTGCGCAACAGAGGCCACGGCCCTGCGCTGGCGGGTG	1967
QY	1046	GCTCTGCCGCACTGAGGGCTTACTACGACGTACTCCCTTGTGACGGGCTCAGACAGCAGC	1105
Db	1961	ACGGCGGCAAGAGATGCGCTGTACGTGGCCCCAGCGGCCGCTGCAC--CCAAAGTCAACGGC	2019
QY	1106	TGAGAGGCGCGCAATGCTAACAAGCTGGGGCGCTTACACACACCTTCTCCCATTTAGGGC	1165
Db	2020	CTGGGCAAGCGCCACGTCGTCCGGACTCGGGCGGCGCGCGCTGTCAACATCAAGGCC	2079
QY	1166	AGCACTGCTTCAAGCCGACGGCGCTTCCGGGCTATGCGTGAAGGGTCTTCAACGAGCCCC	1225
Db	2080	CGCGGGGCGGGGTGCGACGGTGACGTACGAGACGGGTGAAGAGACCTTGGGAGCGGG	2139
QY	1226	CTGGTACCCCTTACCGCGCAGCACATTGACAGCTTCTTTCAACAAAGCGACATGCAAC	1285
Db	2140	ATTCGGGGGCGCGAGCTGAG-----CCGGGGTTTCAACC	2173
QY	1286	TGTGTGACTTACTTACACCCCAAGGCGGACACAGTGTATACCGCGCATGGAAGGGCAGCT	1345
Db	2174	AGGGCGCACAGCTGGACCGGGGCAAGGCGGGGGCGCTGTATCAGACGGCAAGCTGTACCTGTG	2233
QY	1346	ACACCGCGGACGAGGACTGTCACTTACAGCTGGGCTGTGCTCTGTGCGGACGCGCAAGG	1405
Db	2234	CGCGGAGCGGGGATTAACCGGATCTCGGTCAAGGCCACCGCGGTGCTACGCGGAGCGTGAG-	2292
QY	1406	CGTACGTGAGACGACCACTGCTGTGTGACAAACGCCAACGAAGGTCCCGGCGATGTGCT	1465
Db	2293	-----CTGGGACGCCACA	2305
QY	1466	TTCTTGGCTCCGCCACCGCGGAGAGAGGGGCGCATCATCTCTCAAGGGCAACAGT	1525
Db	2306	CCATCTGAGGGCGGTGACAGTTTACGGCAAGGTGACAGCCCGCTCTCAAGCTGACACAAAG	2365
QY	1526	ACAGTTTCAAGATGAGATTTGGGTTCGCGAACCCACATACACCTTCAAGGGCGGACACATCG	1585
Db	2366	GCAAGCCAAAGCT-----CAGCATCTCGGGCTTCCGATGA	2401
QY	1586	TCCCGGCGCACAGGCTCCTTCCGCTCGGCGGGCTGCAAGGTCTATTACAGCACAGGCCGAAA	1645
Db	2402	GCGCGACGCGGCTCTCCCTGAGACTGGGTGGGTGACCGCGGAGGACGCCACCGCGACGA	2461
QY	1646	TGCAAAAGTCCGTGCGCCCTGCCCAAGGACGACGACCGAGTCACTCTGCGCGGGCTTGA	1705

Dd	2462	TCGCGAAGGCGGTGGAGTGGCGCGCGGAAGGCCCGTACGGGCATCGTTCGCG-----	2514
Qy	1706	ACGCCGATGGGAGACAGAGGGGCGCCGACCGCGAGCATGAAGCTCCCGCGCTGTGG	1765
Dd	2515	--TACGACGACGACCGACGAGGGCGCTGACCGCTCGGAACCTGTGCGTGC GGSTACGAGG	2572
Qy	1766	ACCACCTATTGGCCGAGCTGGCGCGCGCGGAACCCAAACCAACCTGCTGTCATGCAAGCGG	1825
Dd	2573	ACAACTGATGTGCGCGGCTGCCGACGACCGAACCAGAACGATGCTGGTCCCAACACCG	2632
Qy	1826	GCACCCCGGAGAGATGCTCCGTGGCTCACGCCACGCGCCCGCATCCAGGCGCTGTACG	1885
Dd	2633	GTTGGTGGTGTCTATGCTCGGTGGGTGTGCCAAGAACCGCGCGGTCTCGAATGTGTGTAAC	2692
Qy	1886	GGCGCACGAGACGGGCGCACTCCATTGCGGAGCTCCTCTTTGGCACTAACCCCTCGG	1945
Dd	2693	CGGGCGAAGCGGGCGCGGACGACGCGCGCGCTGTACGCTACGTAACCGGACCG	2752
Qy	1946	GCAAGCTGTCCCTCAGCTTC-----CCAAAGGCGCTGAGAGCAACCCCGTTCACA	1999
Dd	2753	GCAAGCTACCGCAAGCTTCCTCCGCGCGCGAGAACGACGACCGCTGCGCGACCGCA	2812
Qy	2000	ACTTCGCAACCGAGCGCGGCGGACGCT--GTACGGCGAGAGAGCTACGTCGGGTACA	2056
Dd	2813	ACCGCTACCGCGGCGGTGCACACACAGACAGCTACAGCAGGAGCTACCGCGGGTACC	2872
Qy	2057	GGTACTACGAGTTTGGCGACAGAGCTCAATTTCCTTTGGCCAGGCGCTGTCTACA	2116
Dd	2873	GCTGGTGTGAAAGAGAGAGCTCAAGCGCTGTTCCTCGGTCGCGGACGCGCTGTCTACA	2932
Qy	2117	CCACTTTTGGCTTTCCAAATCTCTCCGTGTCTACAAAGAAC--GGCAAGCTGACCGTGT	2173
Dd	2933	CCTGTTTACGACAGAGGCGCCGACCGTGTGTGGACGTCACAGGCGCGCTGTAAAGTCA	2992
Qy	2174	CCCTCTCCGTGAGAGACACCGGCTCCGTGCGCGGCGACAGGTGGCCACGCTTACGTCA	2233
Dd	2993	CGGTACGGGTGCGGCAACAGGGGCGACGCGCGGCGAGGAGGTCTCTACAGCGTATCTCG	3052
Qy	2234	AGCCCTTCGAAGCGGCGCAATTAACCGCGCGGTCAAGGAGCTCAAGGCTTCCGAAGG	2293
Dd	3053	GGCGGAGCGCGAAGGTGACGCGCTCCGACGAGCGGAGAGAAGAGTCTGTGGGCTACAGAA	3112
Qy	2294	TCGAAGTGCAGCGCGCGGAGACGAGGCGGTGAC	2327
Dd	3113	TCGGCTGCGCGGCGGAGTGCAGAACGCGTAC	3146
RESULT 2			
US-09-320-878-20			
Sequence 20, Application US/09320878A			
Patent No. 6117659			
GENERAL INFORMATION:			
APPLICANT: ASHLEY, Gary			
APPLICANT: BETLACH, Melanie C.			
APPLICANT: BETLACH, Mary C.			
APPLICANT: MCDANIEL, Robert			
APPLICANT: TANG, Li			
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE			
FILE REFERENCE: 300622002120			
CURRENT APPLICATION NUMBER: US/09/320, 878A			
EARLIER FILING DATE: 1999-05-27			
EARLIER APPLICATION NUMBER: CIP OF 09/141, 908			
EARLIER FILING DATE: 1998-08-28			
EARLIER APPLICATION NUMBER: CIP OF 09/073, 538			
EARLIER FILING DATE: 1998-05-06			
EARLIER APPLICATION NUMBER: CIP OF 08/846, 247			
EARLIER FILING DATE: 1997-04-30			
EARLIER APPLICATION NUMBER: 60/119, 139			
EARLIER FILING DATE: 1999-02-08			
EARLIER APPLICATION NUMBER: 60/100, 880			
EARLIER FILING DATE: 1998-09-22			
EARLIER APPLICATION NUMBER: 60/087, 080			

EARLIER FILING DATE: 1998-05-28  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 20  
 LENGTH: 2401  
 TYPE: DNA  
 ORGANISM: Streptomyces venezuelae  
 US-09-320-878-20

Query Match 7.2% Score 179; DB 3; Length 2401;  
 Best Local Similarity 47.7%; Pred. No. 8.5e-30;  
 Matches 1018; Conservative 0; Mismatches 966; Indels 150; Gaps 11;

QY 206 CGCTGGTTCACATTCACCAACCTGCTGCTGAAGAGGAGCAAGATGATGAGGCAAG 265  
 DB 255 CCGTGGCAGACCTTCGAGAGACATGAGCCGACACACTAGCGGAAGTATGAGCGCGC 314  
 QY 266 AGGCGATCGTAAAGTGGCGATGATCTCGGCGCGACTATCAACATCAAGCTCC 325  
 DB 315 ACGGTGCGGCGCTCAACAGACATGCTCGGCGCGAGATGAAACATCATCGGCTGC 374  
 QY 326 CTCTGGTGGACGTGGCTGAGTGCATGTTGATGAGATCCGTTCTGCGGCGTGGAG 385  
 DB 375 CGCAGCGGCGCGGACCTAGACCTTCAGCGAGACCCCTGCTCTCTCGCGCACG 434  
 QY 386 CTGCGGCTCTCATCCGCGGATTCAGACACTGAGTGCAGGCTACGATCAACACTTTT 445  
 DB 435 CGGTGCGCGAGATCAAGGAGCATCCAGGGTGGGCTGATGACACGCGCAACGACTTGG 494  
 QY 446 TGTGATGATCAGAGAGACAGCGCATGATGTTGTCAGACATCTGTCAGGAGCGGCTC 505  
 DB 495 CGGCGCAACCAAGAGAAACACCGCTTCCTGTAAGCGCAATGTCAGACAGACAGCGC 554  
 QY 506 TCCGTAATCTAGCACTCCGCTCCAGATGCTGTGAGACTCCACCGCGGCTGCT 565  
 DB 555 TCCGCGAGATGAGTCCCGCGCTTCGAG---GCTCTCTCAAGCGCGCGGCGCTCT 611  
 QY 566 TCATGAGCGGTACATGAGCATGATGCGTGTGTCAGACAGAAACCTTAAATATCTTG 625  
 DB 612 TCATGTGCTTCAACGCGCTCAAGGAAAGCGTCTCGGAAACGAGAGAGTCTCTCA 671  
 QY 626 ATGGAGTCTTCGAAAGATGGGTTGGATGGCTAATCATGAGGAGTGTAGGCA 685  
 DB 672 ACAAGTGTGCGGACGACGAGTGGGCTTCAGAGGCTGGATGTCTGACTGTGCTCCCA 731  
 QY 686 CATACAGTACACAGAGACGCTGTGCGAGGCTCGACCTCGAGATCCCGGACCTCCAC 745  
 DB 732 C---CCGCGGACCGAGCATCAACAGGCGCTCGACACAGGATG-----775  
 QY 746 GCTTCGAGGAGAAACACTCAAGTTCAGGTCTCCAAAGGAAAGCCCTTATCCAGTCA 805  
 DB 776 -----GGGTTCGAGCTCCCGCGGACGTCGCCGAAGGCGAGCCCTCCCGCGCCA 827  
 QY 806 TTGACAGAGGGGTAGGAGTCTTCAAGTTCGCAAGAGTGTGCTCTCCGAGATGA 855  
 DB 828 AGTTCCTGGGGA---GGCGTGAAGAGCGCGCTCTGAAGGCGACGCTCCCGAGGCG 884  
 QY 866 CGGAGAACGCGCCGAGAGCACTGTCAACAACACCCCGAAGAGGCGAGCTCTCTCGGA 925  
 DB 885 CCGTGAAGCGGTGGGAGGAGATCTCGGCCAGATGAGAGATGTGCTGCTCTCGC 944  
 QY 926 AGTTGGCAAGAGGCGATGTGCTGTGAAGAGAGAAACAGTTTGCCTTGAGCA 985  
 DB 945 CCACTCCGCGCGCGCGCGAGAGCGACAAAGGCGGCTGCCAGGCGGTCTCCCGCAAG 1004  
 QY 986 AGAAGAGAGAGCGCTATGTGCGCCCGCAAGCGCAAGCGACATACACAGGCGGAG 1045  
 DB 1005 TCGCGGAGAGCGCGGTGCTCTGTGCAACAGAGGCGCGCGCTTCGCGCGGTG 1064  
 QY 1046 GCTTCGCGCACTAGGAGCTTACTAGCACTCACTCCCTTGAAGGCGCTAGCAAGAGC 1105  
 DB 1065 ACGCGCGAGAGCATGTGCGGTATGCGCGCGAGCGCGCTGAC-CCCAAGTCAACGCGC 1123

QY 1106 TCGAGAGCGCGCCATGTACACCGTGGCGCTTACACACCGCTCTCCATCTAGGCG 1165  
 DB 1124 CTGGGAGCGCCACGCTCTGCTCCCGAGCTCGCGGCGCGCCACTGTACACCACTAAGGCC 1183  
 QY 1166 AGAGTGTCTACGCGCGGAGCGGCTCCGCGCATGGGCTGAGAGGCTTCAACAGAGCCC 1225  
 DB 1184 CGGCGGCTGGCGGTGCGAGGAGTACGAGACGCGGTGAGAGACCTTCGCGAGCGAG 1243  
 QY 1226 CTGTACCCCTTAACCGCGCACATGACGAGCTCTTCTTCAACAAAGACATGACACC 1285  
 DB 1244 ATCCCGCGCGGAGACCTTCAGC-----CCGCGCTTCACCC 1277  
 QY 1286 TGTGTGACTACTACCAACCCCAAGGCGGAGACAGCTGTACCGCGACATGAGGCGACGT 1345  
 DB 1278 AGGAGCCACAGCTCGAGCGGCGGCAAGGCGGCGGCGGTGATACAGGACAGCTGACCGTGC 1337  
 QY 1346 ACACCGCGCGAGAGAGCTGACCTACGAGCTGGGCTGTGCTGTGCGGACAGCGCAAGG 1405  
 DB 1338 CGCGCGACGCGGAGTACCCATCTCGCGCTGCTGCCACCGGTGATTACGCGCAGGTGAG- 1396  
 QY 1406 CGTACGTAGACGACAGCTGCTGTGACACAGCGCCCAAGCAGGTCGCCGCGATGCT 1465  
 DB 1397 -----CTCGGACGACCA 1409  
 QY 1466 TCTTGGCTCCGCGACCCGCGAGAGACGCGCGCATCATCTGTCAAGGCGCAACGCT 1525  
 DB 1410 CCATCGAGGCGCGGTGAGTCTGAGCAAGTGAAGAGCGCGCTGCTCAAGTGTACCAAGG 1469  
 QY 1526 ACAGTTCAAGATGAGTGGCTCGCGCACCACTACACCTTCAAGGCGGACACATCG 1585  
 DB 1470 GCAAGGACAAAGT-----CAGCATCTCGGCTTGGGATGA 1505  
 QY 1586 TCCCGCGCGACGCGCTCCCGTGGCGGCTGCAAGGTCAATGACGACAGCGGAGAA 1645  
 DB 1506 GTGCCACCCCGCTCTCTCGAGAGTGGCTGGGTAAAGCGCGCGCGCGCGGACGAGCA 1565  
 QY 1646 TCGAAAGTCCGTGCGCTCGCCCAAGAGACGACGAGTCAATCTGCGCGGCGCTTTA 1705  
 DB 1566 TCGCGAAGCGCGGTGAGTGGCGGAGAGCGCGTACGCGGCTGCTCGC-----1617  
 QY 1706 ACGCCGACTGGAGACCGAGGCGCGCGAGCGCGGAGCATGAAGCTCCCGCGGCTGG 1765  
 DB 1618 -CTACAGCAGCGCACCGAGGCGGTGACCTGTCCGAACCTGTGCGCGGCTTACGACAG 1676  
 QY 1766 ACCAGCTATTGCGCGAGCGCGCGCGCGAGACCAACACCTGCTGCTGATGACGAGCG 1825  
 DB 1677 ACAGGTGATGTGCGGTGTGCGGAGAGCCAGACCGAGACGATGCTGCTCAACACCG 1736  
 QY 1826 GCAACCCGAGAGATGCTGCTGCTGACGCGACGCGCGCTCATCCAGGCTGTGAGC 1885  
 DB 1737 GTTCGTGCGGTGATGCGGTGCTGCTCCAGACCGCGCGCTGCTGAGCATGTGATCC 1796  
 QY 1886 GCGGCAAGAGACGGGCACTCATTTGCGGAGCTGTGCTTGGCGACTCAACCCCTGG 1945  
 DB 1797 CGGCGAGGCGGCGCGCGAGGCGACGCGCGCTGCTTACGCTGACGTCAACCGGAGCG 1856  
 QY 1946 GCAAGCTGTCCCTCACTTCC-----AAGCGCTGACGAGCAACCCCGGTTTC 1996  
 DB 1857 GCAAGCTACGAGACACTTCCCGCGCGCGAGAACAGAGACGCGGCGCGCGAGCCGA 1916  
 QY 1997 TCACTTCCGACCGAGCGCGCGCGCGAGCTGTAGCGGAGAGAGTCTGAGTGGGTACA 2056  
 DB 1917 CCAGCTACCGCGCGGTGCAACACAGCAACGCTACGCGGAGGCAATCCACTCGGCTACC 1976  
 QY 2057 GGACTACGAGTGTGCGGCAAGGAGCGTCAATTCCTTGGCGAGCGCTGTCTCA 2116  
 DB 1977 GTGTGTGACAAAGAGAGAGTCAAGCGCTGTCCGTTGCGGACAGGCTGTGTGTA 2036  
 QY 2117 CCAGTTCCTTTTCAATCTCTCGGTCTCACAAAGAC---GGCAAGTACGAGCTGT 2173  
 DB 2037 CCGTGTACGAGAGCGCGCGCGCGAGCGGTGTGCTGACGTCACAGGCTGTGTAAGGTCA 2096  
 QY 2174 CCCTCTCGTGAAGAACACCGGCTCGGTGCGCGGCGCACAGGTGCGCCACGCTCTACGTCA 2233

Db 2097 CGGTGACGGTCCGCAACACGCGGGAAGCGCGCCGAGAGGTCTCCAGGCGTACTCG 2156  
 Oy 2234 AGCCCTCCAGCGCGCAAGATTAAACGCCCGCTCAAGAGCTCAAGGCTTCGCAAG 2293  
 Db 2157 GTCCAGCGCGCAAGCTGAGCGGTCCGCAAGAGAAAGCTGTGGCTACAGCAAG 2216  
 Oy 2294 TCGAAGTCCAGCGCGCGAGAGAGCGGTGAC 2327  
 Db 2217 TCTCGCTCCGCGCGCGAGGCGCAAGACGCTGAC 2250

## RESULT 3

US-09-105-537-23  
 ; Sequence 23, Application US/09105537A

; Patent No. 6255202  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sherman, D.H.  
 ; APPLICANT: Liu, H.  
 ; APPLICANT: Xue, Y.  
 ; APPLICANT: Zhao, L.  
 ; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
 ; FILE REFERENCE: 600,438051  
 ; CURRENT APPLICATION NUMBER: US/09/105,537A  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 23  
 ; LENGTH: 2430  
 ; TYPE: DNA  
 ; ORGANISM: Streptomyces venezuelae  
 ; US-09-105-537-23

Query Match 7.0%; Score 175.2; DB 4; Length 2430;  
 Best Local Similarity 47.6%; Pred. No. 5,6e+29;  
 Matches 1016; Conservative 0; Mismatches 968; Indels 150; Gaps 11;

Oy 206 CGCTCGGTTCCACATTCAACCAACTCTCTCGAAGAGGCGAGTAAGATGAGCGCAAG 265  
 Db 353 CCTGCGCAGACCTTCGACGACACCATGCGCGACAGTACGCAAGGTCTATGGCGCGC 412  
 Oy 266 AGCCCATTCGTAAGATGGCGCATGTATCTCGGCCGCTATCAACATGCAACGCTCC 325  
 Db 413 ACGGTCGCGGCTCAACCAAGGATGCTCTGGCCCGCTATCAACATGCAACGCTCC 472  
 Oy 326 CTCTCGGTGACGTGGCTTCGAGTCTGATGTGAGGATCCGTCTCGCGGCTTGGAG 385  
 Db 473 CGACGCGCGCGCGAGACTACGAGACCTTCAGGAGGAGACCCCTGTCTCTCGCGACG 532  
 Oy 386 CTGCGGCTCTCATCCGCGCATTCAGAGCATGAGTSCAGGCTACGATCAACACTTTT 445  
 Db 533 CGGTCCCGCATCAAGGCGCATTCAGGCTGCTGATGACCAAGGCGCAAGCACTTCG 592  
 Oy 446 TGTGCAATGATCGAGGAGGAGGCGCATGATGTGCAAGCATGTCAGGAGCGGCGTC 505  
 Db 593 CGGCAACAACACGAGAAACACCGCTCTCCGTGAACCCATGTGACGAGACGACG 652  
 Oy 506 TCCGTAATCTAGGCACTCCGTTCCAGATTGCTGTGAGAGACTCCACCGGCTGCT 565  
 Db 653 TCGCGAGATCGAGTTCCCGGGGCTTCAG--GCGTCTCAAGGCGCGGCGCTCT 709  
 Oy 566 TCAATGAGCGGTACATGCGATCATGCGGTCTGTGACGCGAAGCCCTAATATCTTG 625  
 Db 710 TCAATGTGTCTCAACGCGCTTCACGGAAGCGCTCTGCGGCAACGAGGCTCTCA 769  
 Oy 626 ATGAGGATGTTGGAAGGATGGGTTGGAGTGGCTTATCATGAGCGAGCTGACGCA 685  
 Db 770 ACAAGTGTCTGCGACGAGTGGGCTTCAGAGGCTGGGTGATGTCCAGCTGCTGCA 829  
 Oy 686 CATACAGTACAGAGGCGGTGTGGAGGCGCTGACCTCGAGTGGCCGAGCTCCAC 745  
 Db 830 C---CCGCGGACGAGCGCATCACCAGGCGCTCGACAGGAGATG----- 873

Oy 746 GCTCCGAGAGAAACATCAATTCAAGCTCTCCAAAGCAAGAACCTTATCCPGCTCA 805  
 Db 874 -----GGCGTACGATCCCGCGGACGATCCCGAGGCGAGCCCTCCGCCJCGGCA 925  
 Oy 806 TTGACAGAGGCTAGGAAATTCTTACGTTCTGCAAGAAAGTGTGCTCCGAGGTGA 865  
 Db 926 AGTTCTTGGCGA--GCGCTGAAGAGCGCGCTCTGAAGGAGCGGTCCCGAGCGG 962  
 Oy 866 CGGAAAGCGCGCGAGACGATCTCAACAACACCCCGAAGCGGAGCTCTCCGGA 935  
 Db 983 CCGTACGCGGCTCGCGGAGGAGATCGTCGCGCCAGATGAGAAAGTTGCTGCTCTCG 1042  
 Oy 926 AGGTTGCAACGAGGCGATGCTGCTGTAAGAAAGAAACACGTTCTCCCTTGACA 965  
 Db 1043 CCACCTCCGCGCGCGCGCGCGAGCGGCAAGGCGGCTGCCAGGCTCTCCGCAAG 1102  
 Oy 986 AGAAGAAAGAACCTGATTTCGCGCCCAAGCGCAAGGCGACATPACACGCGGAG 1045  
 Db 1103 TCGCGAGAAAGCGCGCGGTGCTCTGCGCAACGAGGCGCAAGGCTCTCCGCTGCG 1162  
 Oy 1046 GCTCGCGCACTCAGGCGCTACTACGACGATCCTCTTGAAGGCGCTCAGCAAGCAG 1105  
 Db 1163 ACGCCGCAAGAGATCGCGGTCTATCGGCCGAGGCGGCTCGAC-CCCAAGTTCACGCG 1221  
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 Oy 1166 AGCAAGTCCATCAGCGCGCGAGCGGCTCCGCGCATGCGCTGAGAGGCTTCAAGAG 1225  
 Db 1282 CGCGCGGTGCGGTGCGACGCTGACGTACGAGAGGAGTACGAGGACTTCGCGAGCAG 1341  
 Oy 1226 CTGTACCCCTACACCGCGGACGATGACGACTCTTTCACCAAGAGGACATGAC 1285  
 Db 1342 ATCCCGGCGGGAACCTCAGC-----CCGCGCTTCAAC 1375  
 Oy 1286 TGTGAGATCTACTACACCGCGGAGAGGCGGAGACGTTGACCGGATGAGGCGACGT 1345  
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 Db 1436 CGCGCGAGGAGGATGACCGCATTCGCGGTGCGCACCGGCTGTACGCGCAGTGCGAG- 1494  
 Oy 1406 CGTACGTAGACACCAAGCTGCTGCTGCAACAGCCACCAAGCAGGTCCTCCGCGAT 1465  
 Db 1495 -----CTCGGACGCGACA 1507  
 Oy 1466 TCTTGGGCTCGGCAACCGCGAGAGAGCGGCGCATCAATCTGTCGAAGGCAACAGT 1525  
 Db 1508 CCATCGAGCGCGGTACGCTTACGCGAAGGTGAGCAGCGCGCTCTCAAGCTGACCAAG 1567  
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 Db 1568 GCAAGCAACACT-----CAGATCTCGGCTTCGCGATGA 1603  
 Oy 1586 TCCCGGCGCAGGCTCTCTCGCGTTCGCGGCTCAAGGTATTTAGACAGGCGCAAA 1645  
 Db 1604 GTGCGACCCCGCTCTCTCGAGCTGGGTGAGCGCGCGCGGCGGCGCGCGAGCA 1663  
 Oy 1646 TCGAAGATCCGCGCGCTCGCAAGAGCAGACACAGTCAATATGTCGCGGCGCTTA 1705  
 Db 1664 TCGGAGAGCGGTGAGTGTGCGCGGAGAGCGGCTGACGCGGCTGTCTTTCG----- 1715  
 Oy 1706 ACGCCAGTGGAGAGCAGAGGCGCGCACCGCGAGCATGAAAGCTCCCGCGCTGCG 1765  
 Db 1716 -CTACGAGAGCGGAGCGAGGCGCTGCGAGCTGCGCAACCTGCTCCGCTACGAGG 1774  
 Oy 1766 ACAGCTATTGCGAGCTGCGCGCGCGGAGAACCAACACCGTGTGCTATGAGAGCG 1825  
 Db 1775 ACAAGCTGATCTCGGCTGTGCGGAGCGCAACCGCAACAGATGTGCTTCAACACG 1834  
 Oy 1826 GCACCGCGAGAGATGCTGCTGCGACGCGACGCGCGCGCTATCAGGCTGTGAG 1885

Db	1835	GTTCGTGGGTGTCATTCCTCGGTGCTGCCAAGACCCGGGGGTCTCTGGAGCATGTGTAC	1894
QY	1886	GCGCCAAGACGACGGGCACTCATTTGCCAGCTGCTTTTGGCACTAACCCCTCG	1945
Db	1895	CGGGCCAGGGGGGGCCGAGGACCGCCGCGCTGTCTACGGTACGTCACCCGAGCG	1954
QY	1946	GCAGCTGTCCCTTCAGTTTCCCC-----AAGGCTCGAGGACAAACCCGGGTTTC	1996
Db	1955	GCAAGCTACGACAGAGTTTCCCGGGCCGCGAGAACGACGCGGTGCGCGCCGACCGA	2014
QY	1997	TCAACTTCGCGACCGAGGGCCGGCGACGCTGTACGGCGAGAGCTGTACGTGGGTACA	2056
Db	2015	CACGCTACCCGGGGGTGGACAAACGACAGACGTCCGCGAAGGGATCCACTGTGGGTACC	2074
QY	2057	GGTACTACGAGTTTGGCCGACAGGAGCTCAATTTCCCTTTGGCCAGGGCTGTCTACA	2116
Db	2075	GCTGGTTTCGACAGAGAACGTCAACCGCTGTTCCTCGTTCGGGACACGGCTGTGTACA	2134
QY	2117	CCACTTTTGGCTTTTCCAACTCTCCGTGTCTCACAAAGAC---GGCAAGCTGACAGCTGT	2173
Db	2135	CTGTGTTACGACAGAGGGCCCCCGACCGTGTGGTGTACGTCCACGGGTGGTGAAGGTCA	2194
QY	2174	CCCTCTCCGTGAAGAACACCGGCTCTGGTCCGGCCGACACAGGTGGCCAGCTCTACGTCA	2233
Db	2195	CGGTACAGGTCCGACAAAGGGGGGAACGGCCGGCCGACGAGAGGTCTTCACAGGGTACTCG	2254
QY	2234	AGCCCCCTCCAAAGCGGCCAAGATTAACTCCGCCCTCACAAGAGCTCAAGGGCTTTCGCAAAAG	2293
Db	2255	GTCGACAGCCGAAAGTACGCGCTCCGACGGCAGAAAGAAAGCTCTGGGCTTCACGAAAG	2314
QY	2294	TCGAACTGACAGCCCGGGGAGAACGAAAGGGGTGAC	2327
Db	2315	TTCTGCTGCGCGGGGGAGGACAAAGCGGTGAC	2348

```

: RESULT 4
: US-09-105-537-3
: Sequence 3, Application US/09105537A
: Patent No. 6265202
: GENERAL INFORMATION:
: APPLICANT: Sherman, D. H.
: APPLICANT: Liu, H.
: APPLICANT: Xue, Y.
: APPLICANT: Zhao, L.
: TITLE OF INVENTION: DNA encoding methymycin and pikromycin
: FILE REFERENCE: 600.438US1
: CURRENT APPLICATION NUMBER: US/09/105,537A
: CURRENT FILING DATE: 1998-06-26
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 13613
: TYPE: DNA
: ORGANISM: Streptomyces venezuelae
: US-09-105-537-3

```

[illegible]

OY	386	CTGGGGCTTCATCCGGGCGATTCCAGAGCACTGGAGTGCAGGGTACGATCAAGCACTTTT	445
Db	4844	CGGTGCCCCAGATATAAGGGCATCCAGGGTTCGGGTGTGATGACACAGGCCAAGCACTTCG	4903
OY	446	TGTGCATATGATCAGAGAGACAGGCGCATGTATGTGTGACAGAGCATCTGTCACGAGCGGGCTC	505
Db	4904	CGGGCAACAAACACAGAGAGAACACCGGCTTTCGCTGAAGCGCAATGTGCAGACAGAGACGC	4965
OY	506	TCCGTGAATCTACGCACCTCCCTTCACATTTCTGTGGAGACTCCACGCCGGGTGGT	565
Db	4964	TCCCGGAGATGAACTTCCCGCGTTTCAG---CGCTCTCCAAAGGCGGCGGGGCTCTCT	5020
OY	566	TCATAGAGGGGTACAAATGGATCAATGGGTGTGCTGTGACAGCGAGAACCCCTAAATATCTTG	625
Db	5021	TCATGTGTCTTCAACAGGGCTTCAACGGGAAGCGCTCTGTCCGCAACGACAGACTCTCTA	5088
OY	626	ATGGGATGCTTCGAAGAAGTAATGGGGTTGGGATGGCCCTAATCATGAGCACTGGTACGGCA	685
Db	5081	ACAACGTCTCTCGACAGCAGTGGGGGCTTCCAGGGCTGGGGTGAATGTCCAGCTGTCTGGCA	5148
OY	686	CATACAGTACCAACAGAAACCGTGTGTGGCAGGCTCCACTCGAGATGCCGGAGCTCCAC	745
Db	5141	C---CCCGGGACCCGAGCGCATCCACAAAGGGCCTCGACACGAGGATG-----	5184
OY	746	GCTTCCGAGGAGAAACAACCTAAGTTCAAGTCCGTCGAACGAGAAAGCCCTTATCCACGTCA	805
Db	5185	-----GGCGTGCAGCTCCCGGGCGAGCTCCGAAGGGCGAGCCCTGCGCGCGGCTCA	5233
OY	806	TTGACACAGAGGGCTAGGGAGTTCTTCATGTCTCAAGAAGTGTGCTGCCCTCGGAGTGA	865
Db	5237	AGTTCTTCGGGGA---GGCGGTGAAGACGGCGCTCTCGAAACGGCACAGTGTCCCGAGGGG	5295
OY	866	CGGAGAACGGCCCCGAGACGACTGTCAACAACACCCCGAAACGGCAGCTCTCTCCGGA	925
Db	5294	CCGTGACCGCGTCCGGCGAGGGGATCTCGCCGACGATGGAGAACTTCGGTCTGCTCTCG	5355
OY	926	AGGTTGGCAAGAGGGGCGATGTGTGTGAAAGCAAGAAACAAGCTTTCGGCTTGAGA	985
Db	5354	CCACTCCGGCGCCCGCGGCGGAGCGCACAAAGGCGGGTGGCCAGGGGCTGTCCCGCAAGG	5411
OY	986	AGAAGAAGAAACGCTGATTTGTGGGCCCAACGCCCAAGCAGGCACATCTACACGGCGGAG	1045
Db	5414	TGCGCGAAGAACGGGCGGTGCTCTGTGGCAACAGAGGCCAGGCGCTTCGCGCTCGCGGGT	5477
OY	1046	GCTCTGCCGCACCTGAGGGGCTTACTACGACATCACTCCCTTGTACGGGCTCAGACAAGAC	1105
Db	5474	ACGCGGGCAAGAGCATCGCGGTATCTGGCCGACGCGCGCTGCACACACATCTCAAGGCTC	5533
OY	1106	TCGAGACGCCGCATCTGTACACGCTCGGGGCTCTACACACACCTTCTCCCATTTAGGGC	1165
Db	5533	CTGGGCACCGCCGACGTCGTCCCGGACTCGGCGGGGCGCCACTGTCAACACATCTCAAGGCTC	5592
OY	1166	AGCAAGTGTCTACGCGCCGAGGGGCTCTCGGGCATTGGGTGGAGGGTCTTCAACGAGAGCC	1225
Db	5593	CGCGGGGTGTGGGTGTGAGGGTGTACTACGAACGGGTGAGGAGACTTTCGGAGCGCAG	5655
OY	1226	CTGGTACCCCTTAACCGCCAGACATTGACAGGCTCTTCTTCAACACAGACGGAATGACCC	1285
Db	5653	ATTCGGGGGGGGAACCTCAG-----CCGGGCTTCAACC	5688
OY	1286	TGTGTGACTTACTACACCCCAAGGCGGACAGACGTTGTATACGCCGATGAGAGGGCAGCT	1345
Db	5687	AGGGCACCACTGAGACCGGGACGCGGGGCGCTGTACGACGGCACGCTGACCGTGC	5748
OY	1346	ACACGCCGAGAGGAGACTGTGACCTTAGAGCTGGGGCTCGTCGTTCGGGCAAGGGCAAGG	1405
Db	5747	CGCGCGAGGGGAGTATCCGATCGCGGTCCGTGCACCGGTGGTTACCGGACGGTGCAG-	5805
OY	1406	GTAGTGTAGACGACCACTGTGTGTGACAAACGCCAACGAAGAGGTCCCGCGCATGTGCT	1465
Db	5806	-----CTCGGCAACCCACA	5818
OY	1466	TCCTTGGCTCCGCCACCCGAGAGAGACGGGCGCATCAATCTCTGTCAAGGGCAACAGCT	1525





Db 218227 GAATCGGGTGTGGC-----GTTGCTGGATTCGAGGGGTGACAGCTCGAACCC 218274  
QY 2308 GCGGAGCGAAGCGCGTGCATATCGAGAGAGAGAGACTGCTCCGTATTTTGAT 2367  
Db 218275 GGCAGACTCGGGGTAAAGATCGAGGGCGCCGACTGCTCCCGCTACGAGGCG 218334  
QY 2368 GAGG 2371  
Db 218335 GAGG 218338

## RESULT 8

US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 4.58; Score 111.6; DB 4; Length 4411529;  
Best Local Similarity 52.08; Pred. No. 1.6e-14;  
Matches 345; Conservative 0; Mismatches 289; Indels 30; Gaps 3;

QY 1723 GAGGCGCGCAGCGCGAGACATGAAGCTCCCGCGTGTGGACGACTATTCGCGAC 1782  
Db 217581 GAGGCGCTTCGACAGCGCGCATCTGTCTGCATGGGTGATGAGATCGCTGATCGCGCA 217640  
QY 1783 GTGGCGCGCGCGAACCAGACCGCTGTCTGATGACGAGGCGACCCCGGAGAGATG 1842  
Db 217641 GTGCGGTCTCGCAACGCGATATCGCTGTGTGAGAGGCGGCGCGGTGACCAAG 217700  
QY 1843 CCTGCGCTCAGCGCGACCGCGCTGATCCAGGCGCTGATGAGCGCGCAAGAGAGGCG 1902  
Db 217701 CCTGCGCGCTGAGCGCGCATATGACGCGCTGATTCGCGCGCGCGGCGGTGCG 217760  
QY 1903 AACTCATTGCGCGAGCTGTCTTTGGGACTACACCCCTCGGCGAAGTGTCTCAGC 1962  
Db 217761 CAGGCGCTTGGGAGATGTGACCGCGAGTGAATCTTCGGCGCGCGCGATCAGC 217820  
QY 1963 TTCCCGCAGCGCGCTGCGAGCAACCCCGGCTTCTCACTTCGCGACCGAGCGCGCGC- 2021  
Db 217821 TTCCCGGCTGATCTCGGTGAGACGCGCTCGCAACCCCGCGAGGTGCGCGCGGTG 217880  
QY 2022 -----CAGCGTACGGGAGGAGGAGTCTACGTGGGAGACAGTACTACGAG 2067  
Db 217881 GGGACATGACACGATGCTACACCGAGGCGCGAGTGTGTTACGCTGTTGGC 217940  
QY 2068 TTGGCGCAGAGCGATTCCTTGGCGACGCGCTGTCTACACACTTTTGGC 2127  
Db 217941 AGCACAATAGACCCCGAGTTCGCTTGGCTGACGCGCTTGTCTATACCACTTTGCGAG 218000  
QY 2128 TTTTCCATCTCTCCGTCTCTACAGAGAGCGAGTGAAGTGTCTCTCTCTCTCTGAG 2187  
Db 218001 TATCGTACCTGTGTGTGAGGCGC---GGCGACACGCTGACGCGCGATTCACGCTTAC 218057  
QY 2188 AACACGCGCTCGCGCGCGAGAGGTGGCGGAGCTTACGTCAGACCCCTCCAGCG 2247

Db 218058 AACACGCGCGACCGCGAGCGGGCGAGTGTCCCGCACTGTATATGATCCAGCTCCGCGC 218117  
QY 2248 GCCAAGATTAAACCGCCCGCTCAAGAGGCTTCGCAAGAGTGCAGACTCGACGCC 2307  
Db 218118 GAATGCGCGTTCG-----GTTGCTGGATTCGAGCGGGGTGACACTCGAACCC 218165  
QY 2308 GCGGAGCGAAGCGCGTGCATTCGAGAGAGAGAGAAAGTACGTGCTGCTATTTTGAT 2367  
Db 218166 GGCAGACTCGCGGGGTAAAGATCGAGGCGCGACCGCGACTGCTCGCCCGCTACGAGCGC 218225  
QY 2368 GAGG 2371  
Db 218226 GAGG 218229

## RESULT 9

US-09-147-236-1  
; Sequence 1, Application US/09147236A  
; Patent No. 6316251  
; GENERAL INFORMATION:  
; APPLICANT: TONOUCHI, Naoto  
; APPLICANT: TSUCHIDA, Takayasu  
; APPLICANT: YOSHINAGA, Fumihito  
; APPLICANT: TAHARA, Naoki  
; APPLICANT: HAYASHI, Takahisa  
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE  
; FILE REFERENCE: 6537-011-0PCT  
; CURRENT APPLICATION NUMBER: US/09/147,236A  
; CURRENT FILING DATE: 1999-04-08  
; EARLIER APPLICATION NUMBER: PCT/JP97/03633  
; EARLIER FILING DATE: 1997-10-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 16836  
; TYPE: DNA  
; ORGANISM: Acetobacter xylinum

QY 1723 GAGGCGCGCAGCGCGAGACATGAAGCTCCCGCGTGTGGACGACTATTCGCGAC 1782  
Db 217581 GAGGCGCTTCGACAGCGCGCATCTGTCTGCATGGGTGATGAGATCGCTGATCGCGCA 217640  
QY 1783 GTGGCGCGCGCGAACCAGACCGCTGTCTGATGACGAGGCGACCCCGGAGAGATG 1842  
Db 217641 GTGCGGTCTCGCAACGCGATATCGCTGTGTGAGAGGCGGCGCGGTGACCAAG 217700  
QY 1843 CCTGCGCTCAGCGCGACCGCGCTGATCCAGGCGCTGATGAGCGCGCGCAAGAGAGGCG 1902  
Db 217701 CCTGCGCGCTGAGCGCGCATATGACGCGCTGATTCGCGCGCGCGGCGGTGCG 217760  
QY 1903 AACTCATTGCGCGAGCTGTCTTTGGGACTACACCCCTCGGCGAAGTGTCTCAGC 1962  
Db 217761 CAGGCGCTTGGGAGATGTGACCGCGAGTGAATCTTCGGCGCGCGCGATCAGC 217820  
QY 1963 TTCCCGCAGCGCGCTGCGAGCAACCCCGGCTTCTCACTTCGCGACCGAGCGCGCGC- 2021  
Db 217821 TTCCCGGCTGATCTCGGTGAGACGCGCTCGCAACCCCGCGAGGTGCGCGCGGTG 217880  
QY 2022 -----CAGCGTACGGGAGGAGGAGTCTACGTGGGAGACAGTACTACGAG 2067  
Db 217881 GGGACATGACACGATGCTACACCGAGGCGCGAGTGTGTTACGCTGTTGGC 217940  
QY 2068 TTGGCGCAGAGCGATTCCTTGGCGACGCGCTGTCTACACACTTTTGGC 2127  
Db 217941 AGCACAATAGACCCCGAGTTCGCTTGGCTGACGCGCTTGTCTATACCACTTTGCGAG 218000  
QY 2128 TTTTCCATCTCTCCGTCTCTACAGAGAGCGAGTGAAGTGTCTCTCTCTCTCTGAG 2187  
Db 218001 TATCGTACCTGTGTGTGAGGCGC---GGCGACACGCTGACGCGCGATTCACGCTTAC 218057  
QY 2188 AACACGCGCTCGCGCGCGAGAGGTGGCGGAGCTTACGTCAGACCCCTCCAGCG 2247

Query Match 4.18; Score 101.4; DB 4; Length 16836;  
Best Local Similarity 50.58; Pred. No. 6.6e-13;  
Matches 246; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

QY 242 AGCGAGTAAAGTAAAGGCGCAAGAGCGCATCGCTAAGAGTGGCGCATGATCTCGGCGC 301  
Db 12845 AGCGCGGTGTCAATGATGCGGCGCGAGCATGAGAGCGCGCTTCAACATCTGCTTGGCG 12904  
QY 302 CGACTATCAACATGCAAGCTTCCTCTCGGTGAGCGTGGCTTGCAGTGTGAGGAG 361  
Db 12905 GCGGTGCGGACTGACGCGCGACCGCGCGTGGCGCGCGCACTTTGAATATGCGGGCGAAG 12964  
QY 362 ATCGTCTCTGCGGCGGCTTGGAGCTGCGCTTCATCCGCGGCAATTCAGAGCACTGAG 421



Db 12965 ATCCGCTGACAGCCGGGCGCATGTTGGGACAGCACCATTGAGGGGTCCAGTCCGACATG 13024  
QY 422 TGCAGGCTACGATCAAGCACTTTTGTGCAATGATCAGAGAGACAGCGCATGATGCTGC 481  
Db 13025 TGATCTCCAGCCTAAGCATTTATGCGATGATGACCTGCAAACTCGCGCATGACCATTA 13084  
QY 482 AGAGCATGCTACAGGAGCGGCTCTCCGTGAATCTACGACCTCCGTTCCAGATTGCTG 541  
Db 13085 GCGCGATATGACCTCTGTGTCATGCGTGAAGCAGCTGCTGGCTTCGAGATCCGCG 13144  
QY 542 TGCAGACTCCAGCCGGGTGCTTTCATGACGGGTACAAATGATGATGATGCTGCT 601  
Db 13145 TTGAACCGGGGATCCGGGCGGTCATGCTGTACAAACCGGCTCAACGACTGTATG 13204  
QY 602 GCAGGAGAACCTTAATATCTTGTATGATGATGCTTTCGAAAGAAATGGGTTGGGATGACC 661  
Db 13205 CGTGTGAACACCGTACTGCTGTAACAAGACGCTGAAGCAGGACTGGCATTTATCCGGCT 13264  
QY 662 TAATCATGAGCGACTGTGACGACATACAGTACCACAGAAAGCCGTTTGGCAGGCTCG 721  
Db 13265 TTGTCATGTCGACTGAGGGGGGCGACGATCTCCGCGGGGCGGCTGCGGGGCTGG 13324  
QY 722 ACCTCGA 728  
Db 13325 ATCAGGA 13331

RESULT 10  
US-09-147-236-10  
; Sequence 10, Application US/09147236A  
; Patent No. 6316251  
; GENERAL INFORMATION:  
; APPLICANT: TONOUCHI, Naoto  
; APPLICANT: TSUCHIDA, Takayasu  
; APPLICANT: YOSHINAGA, Fumihito  
; APPLICANT: TAHARA, Naoki  
; APPLICANT: HAYASHI, Takahisa  
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE  
; FILE REFERENCE: 6537-011-0PCT  
; CURRENT APPLICATION NUMBER: US/09/147,236A  
; CURRENT FILING DATE: 1999-04-08  
; EARLIER APPLICATION NUMBER: PCT/JP97/03633  
; EARLIER FILING DATE: 1997-10-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 16836  
; TYPE: DNA  
; ORGANISM: Acetobacter xylinum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1891)..(2922)  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence is the same as SEQ ID NO:1  
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, c, or  
; OTHER INFORMATION: t  
; OTHER INFORMATION: t  
US-09-147-236-10

Query Match 4.1%; Score 101.4; DB 4; Length 16836;  
Best Local Similarity 50.5%; Pred. No. 6.6e-13;  
Matches 246; Conservative 0; Mismatches 241; Indels 0; Gaps 0;  
QY 242 AGGACAGTAAGATGATGGGCAAGAGGCCATGCTTAAGAGTGGCATGTGATCTCGGCC 301  
Db 12845 AGGCGGCTGTCATGATCGGGCGAGGCGATGGCAGGCGCTTCAACATCCCTGTGGCG 12904  
QY 302 CGACTATCAACAATGCAAGCTCCCTCTCGGNGAGCGTTCGAGTGCATTTGGGAGG 361  
Db 12905 GCGGTGCGGACCTGACGCGCGACCCGCTGGGCGCCGCAACTTTGAATATGGGCGGAG 12964  
QY 362 ATCCGTTCTGGCGGCTTGGGAGCTGCGCTCTCATTCGCGGCAATTCAGAGCACTGGAG 421

Db 12965 ATCCGCTGACAGCCGGGCGCATGTTGGGACAGCACCATTGAGGGCGTCCAGTCCGACATG 13024  
QY 422 TGCAGGCTACGATCAAGCACTTTTGTGCAATGATCAGAGAGACAGCGCATGATGCTGC 481  
Db 13025 TGATCTCCAGCCTAAGCATTTATGCGATGATGACCTGCAAACTCGCGCATGACCATTA 13084  
QY 482 AGAGCATGCTACAGGAGCGGCTCTCCGTGAATCTACGACCTCCGTTCCAGATTGCTG 541  
Db 13085 GCGCGATATGACCTCTGTGTCATGCGTGAAGCAGCTGCTGGCTTCGAGATCCGCG 13144  
QY 542 TGCAGACTCCAGCCGGGTGCTTTCATGACGGGTACAAATGATGATGATGCTGCT 601  
Db 13145 TTGAACCGGGGATCCGGGCGGTCATGCTGTACAAACCGGCTCAACGACTGTATG 13204  
QY 602 GCAGGAGAACCTTAATATCTTGTATGATGATGCTTTCGAAAGAAATGGGTTGGGATGACC 661  
Db 13205 CGTGTGAACACCGTACTGCTGTAACAAGACGCTGAAGCAGGACTGGCATTTATCCGGCT 13264  
QY 662 TAATCATGAGCGACTGTGACGACATACAGTACCACAGAAAGCCGTTTGGCAGGCTCG 721  
Db 13265 TTGTCATGTCGACTGAGGGGGGCGACGATCTCCGCGGGGCGGCTGCGGGGCTGG 13324  
QY 722 ACCTCGA 728  
Db 13325 ATCAGGA 13331

RESULT 11  
US-08-387-942C-1  
; Sequence 1, Application US/08387942C  
; Patent No. 5939289  
; GENERAL INFORMATION:  
; APPLICANT: ERTESVAG, HELGA  
; APPLICANT: VALLA, SYEIN  
; APPLICANT: SKJAK-BRAEK, GUDMUND  
; APPLICANT: LARSEN, BJORN  
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES  
; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP  
; STREET: P.O. BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,942C  
; FILING DATE: 09-May-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1809-106P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-205-8050  
; TELEFAX: 703-205-8050  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12588 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Azotobacter vinelandii  
; STRAIN: E

FEATURE:  
NAME/KEY: CDS  
LOCATION: 290..1951  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2227..6438  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 6702..9695  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 9973..12588  
US-08-387-942C-1

Query Match 3.4%; Score 84.6; DB 2; Length 12588;  
Best Local Similarity 43.3%; Pred. No. 2.5e-09;  
Matches 451; Conservative 0; Mismatches 584; Indels 6; Gaps 1;

QY 1197 CATGCGTGGAGGCTTCTCAACGAGCCCTGTACCCCTAACCCGACACATTGACGA 1256  
DB 2601 CATCCCGGCGACGAGCGGCGCGATCGACAGTGGAGCCGGTGAATCCGCGA 2660  
QY 1257 GCTCTTCTTACCAACGAGCATGACCTGTGTGACTACTACACCCCAAGGCGGACGA 1316  
DB 2661 GATTCGGGTACGAGTTTGACCCCGACAGACACATCAACCTTACATCCGCGACG 2720  
QY 1317 CACGTGTACGCGGACATGAGGCGACGTAACACCGCGACGAGACTGACCTAGAGCT 1376  
DB 2721 CGTGGCGCGACGACACGCTGACGCGCTTCCGCGCGACTACAGGTGGCGGGGTGT 2780  
QY 1377 CGGCGCTGTGTGTGGGCGACGCGCAAGGCGTACGTAGACGACAGCTGTGTGACGA 1436  
DB 2781 CGAGAACAGCTGTCTGTAACACACGACGCGCGCTTCAACATGTCACACGACCAA 2840  
QY 1437 CGGCGACGAGGTCGCGGCGATGCTTCTTGGGCTCGGCGACCGCGGAGAGCGG 1496  
DB 2841 CGACTTCGTCTGAGACAAACAGTCCCTACGCGCAAGCGCGCGCGCTGTGTGCA 2900  
QY 1497 CGGATCAATCTGTCAAGGCGACACGTAACAAGTTCAAGATCGATGCGTCCGACC 1556  
DB 2901 GCGCGGCTGTACGACCTCCCGCATCCACATCTGATGACGCGGCGGCTACTA 2960  
QY 1557 CACCTACACCTCAAGGCGGACACCATCTCCCGCGCGCTCCCTCGGCTGGGCG 1616  
DB 2961 CGACACGCGCTTGAAGGCGTCAAGTATGCGCGACGACGCTTCCGCGCAAGCGC 3020  
QY 1617 CTGCAAGGTCTATGACGACGCGCAATCGAAAAGTCCGCGCTCGCGCAAGAGCA 1676  
DB 3021 CGAGATCTAGGCGAAGCGGCTGTACGCGGTGGCGTCTACGCGCGCGACAGTCAAT 3080  
QY 1677 CGACGAGTCAATCTGTGCGGCGGCTTACCGCGAGTGGGAGCGAGGCGCGGACCG 1736  
DB 3081 CCTCGCAACGACGATTCAGACAAATTCGAGAACGCGCTTATGCGAAGTCTCTCA 3140  
QY 1737 CGCGAGCATAGATCCCGCGGCTGTGACACGCTCAATTCGCGAGTGGCGCGCGAA 1796  
DB 3141 GTCCTACGACGACACCGCGGCGGTGTCCGCGCACTTTTACGTACACCGGACCTGCT 3200  
QY 1797 CCGAAACACGCTGTGTGATGACGAGGCGACCCCGAGAGATGCCCTGTGAGCGC 1856  
DB 3201 CGAAGGCAACGCTATCAGCGGCTCGGCAATTCACATACGCGCATCCAGAGCGGCGCA 3260  
QY 1857 CAGGCGCGCGTATCAGGCGCTGTAGCGGCGCAACGAGAGCGGCACTCATTTGCGGA 1916  
DB 3261 CGGCAACGCTACAGACGCTTACGCAACGACATGACGAGTGTGACAGCGGCGGCT 3320  
QY 1917 GCTGCTTGTGGGCTACACCCCTCGGCGAAGTGTCTCTCAAGCTTCCCAAGCGCT 1976  
DB 3321 AGGCTGTATGCGGCGCACTGACGTTTCCAGCGATGTCGCGCACTGCGCAGCGGAC 3380  
QY 1977 GCAGGACAAACCCGCTTCTCA-----CTTCGACCGAGCGCGGCGCGCGCTGTA 2030  
DB 3381 CCTCGAAGGCGAGCGGCGGCGGCGGCGGCTGTGAGCGGCGACGAGGCGCGACGAGCGTGT 3440

QY 2031 CGGCGAGGACGCTACGTCGCTGCTACAGTACAGTGGTCCGACAGGACGTCAATT 2090  
DB 3441 CGGCGAGGCGCGGCGACGACGACCGCTGACAGCGGATGCGCGCAACGACATCTTCAGCGCGG 3500  
QY 2091 CCCCTTTGGCCACGCGCTGTCTTACACACATTTTCCCTTTTCCATCTCTCCGTCTCA 2150  
DB 3501 GCGAGGCGCGACACATCTGACCGCGCGCGCGCGCGACACCTTCCGCTTCCGCGCG 3560  
QY 2151 CAGGACGCGCAAGTACGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2210  
DB 3561 CAGCGACGCTACGCGACGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3620  
QY 2211 ACAGTGGCGCGGCTCTAGT 2231  
DB 3621 CGACGAGACACGATCGACT 3641

RESULT 12  
US-09-197-649-7  
Sequence 7, Application US/09197649  
Patent No. 6194550  
GENERAL INFORMATION:  
APPLICANT: Gold, Larry  
APPLICANT: Tuerk, Craig  
APPLICANT: Pribnow, David  
APPLICANT: Smith, Jonathan D.  
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation  
FILE REFERENCE: NEX02/CI-CON  
CURRENT APPLICATION NUMBER: US/09/197, 649  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: 07/829, 461  
EARLIER FILING DATE: 1992-01-31  
EARLIER APPLICATION NUMBER: 07/739, 055  
EARLIER FILING DATE: 1991-08-01  
EARLIER APPLICATION NUMBER: 07/561, 968  
EARLIER FILING DATE: 1990-08-02  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 7  
LENGTH: 390  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Sequence  
OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed  
OTHER INFORMATION: fragments having NcoI restriction sites.  
US-09-197-649-7

Query Match 3.4%; Score 84.4; DB 4; Length 390;  
Best Local Similarity 51.9%; Pred. No. 1.2e-09;  
Matches 190; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 1223 GTACGCGACATGAGGCGACGTACACCGCGGAGGAGGAGTACCTACAGCTCGGCT 1382  
DB 8 GAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 67  
QY 1383 GCTGCTGTGGCGCGCAAGGCGTCTAGACGACGACGACGACGACGACGACGACGACGAC 1442  
DB 68 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 127  
QY 1443 CAGCAGGTCCCGGCGATGCTTCTTCCGCTCCGCGACCCGCGAGAGAGAGCGGCGCAT 1502  
DB 128 CGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 187  
QY 1503 CAATCTGTCAAGGCGCAACGTAAGTTCAAGATCGAGTTTCCGCGACCCACCTTA 1562  
DB 188 CGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 247  
QY 1563 CACCTTCAGGCGGACACATCTGCTCCCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCT 1622  
DB 248 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 307



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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625,140
FILING DATE: 10-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dillahunty, T. Gene
REGISTRATION NUMBER: 25,423
REFERENCE/DOCKET NUMBER: 010055-056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
FEATURE:
NAME/KEY: CDS
LOCATION: join(311..375, 446..2205, 2270..2679)
FEATURE:
NAME/KEY: Intron
LOCATION: 376..445
FEATURE:
NAME/KEY: Intron
LOCATION: 2206..2269
US-08-462-090-1

Query Match          3.3%; Score 83.8; DB 3; Length 3033;
Best Local Similarity 50.1%; Pred. No. 2.7e-09;
Matches 264; Conservative 0; Mismatches 257; Indels 6; Gaps 2;

QY 214 TCACATTCAACCAACTGCTGCTGAGAGGAGGAGTATGATGAGGCAAAAGGCCATC 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 720 TCAGAGTGGAGATGTCATTTGATCCCGAAGGAGGAGTATGATGAGGAGGAG 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 274 GCTAAGAGTGGAGTATGATGATGCTGCGCC--GACTATCAACATGCAAGCTCCCTTC 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 780 GCTCGGGGATTCATGTCATCTGCTGCTGCTGCGCCGCTGGGAAGAGCTCCGAG 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 GGTGAGAGTGGCTTTCGATGATGCTGAGATCCGTTCTCGCGGCTTTGGAGCTGCG 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 840 GCGGTCGCAACTGGAGGCGCTCGGTGTCATTCATCTCAGCGGCAATGCCATGGGT 899
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 391 GCTCTATCCGCGGATTCAGAGCACTGAGAGCTGAGGCTAGCATCAACGACTTTTGTGC 450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 900 CAACCATCAACGCGATCCAGTCGAGGCGTGCAGGCGACGCAAGCACTATATCCTC 959
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 451 AATGATCAGGAGGAGGAGGAGGAGTATGATGAGAGATGCTCAGGAGGCGGCTCCGCT 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 960 AAGGAGCAGAGGCTCATGAGAAACCAATTTGAGCAACCCAGATGACCAACTCTCCAT 1019
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 511 GAAATCTAGCACTCCGCTTCAGATTTGCTGTCGAGACTCCAGCGGCTGCTTCATG 570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1020 GACTCTATTAAGTGGCAATTTGCCAGCGGCTTC--AGGCCAATGTGCTTCTGTCATG 1076
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 571 ACGGCTCAAGTGGATTCATGAGCGGTGCTGTCAGCGAGCAACCCCTAATATTTGATGG 630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1077 TGCTCTGAACAGAGGATTCATACCACTTGCGCTGCGAGATCAGTACACGCTGAGACT 1136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 631 ATGCTCTGAAGGAATGAGGAGTGGGATGAGCTAATCATAGAGAGGAGCTGATAGGCAATAC 690
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1137 GTGCTCAAGAGCAGCTGGGGTTCCAGGCTATGTCATAGCAGCTGGAGACGACACAGCAG 1196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 691 AGTACCAAGAGCGCTTGGCAGGCTGTCAGCTGAGAGTCCCGG 737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1197 ACGAGTGTCCAAAGCGCGAATTCGTGGGCTTGGATGTGATGTCAATGCTGAG 1243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 15
US-08-463-461-1
Sequence 1, Application US/08463461
Patent No. 6103464
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Barnett, Christopher C.
APPLICANT: Shoemaker, Sharon
TITLE OF INVENTION: Saccharification of Cellulose by Cloning
TITLE OF INVENTION: and Amplification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Trichoderma Reesei
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,461
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC78D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-846-7555
TELEFAX: 415-845-6504
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
FEATURE:
NAME/KEY: CDS
LOCATION: join(311..375, 446..2205, 2270..2679)
FEATURE:
NAME/KEY: Intron
LOCATION: 376..445
FEATURE:
NAME/KEY: Intron
LOCATION: 2206..2269
US-08-463-461-1

Query Match          3.3%; Score 83.8; DB 3; Length 3033;
Best Local Similarity 50.1%; Pred. No. 2.7e-09;
Matches 264; Conservative 0; Mismatches 257; Indels 6; Gaps 2;

QY 214 TCACATTCAACCAACTGCTGCTGAGAGGAGGAGTATGATGAGGCAAAAGGCCATC 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 720 TCAGAGTGGAGATGTCATTTGATCCCGAAGGAGGAGTATGATGAGGAGGAG 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 274 GCTAAGAGTGGAGTATGATGATGCTGCGCC--GACTATCAACATGCAAGCTCCCTTC 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 780 GCTCGGGGATTCATGTCATCTGCTGCTGCTGCGCCGCTGGGAAGAGCTCCGAG 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 GGTGAGAGTGGCTTTCGATGATGCTGAGATCCGTTCTCGCGGCTTTGGAGCTGCG 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 840 GCGGTCGCAACTGGAGGCGCTCGGTGTCATTCATCTCAGCGGCAATGCCATGGGT 899
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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